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IN THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claims 1-106. (Cancelled).

Claim 107. (Previously presented) A method of testing a sample for the presence of *E. coli* encoding bacterial polysaccharide O-antigen serotype O111, the method comprising the steps of:

- (a) providing a sample to be tested;
- (b) providing at least one oligonucleotide molecule which is about 17 to 28 nucleotides in length, and hybridizes using highly stringent wash conditions, to a nucleic acid sequence selected from the group consisting of:

wbdH (nucleotide positions 739 to 1932 of SEQ ID NO:1);

wzx (nucleotide positions 8646 to 9911 of SEQ ID NO:1)

wzy (nucleotide positions 9901 to 10953 of SEQ ID NO:1); and

wbdM (nucleotide positions 11821 to 12945 of SEQ ID NO:1)

or to at least one nucleic acid sequence complementary to the group consisting of:

wbdH (nucleotide positions 739 to 1932 of SEQ ID NO:1);

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wzx (nucleotide positions 8646 to 9911 of SEQ ID NO:1)

wzy (nucleotide positions 9901 to 10953 of SEQ ID NO:1); and

wbdM (nucleotide positions 11821 to 12945 of SEQ ID NO:1),

- (c) contacting said sample with said at least one oligonucleotide molecule to permit said oligonucleotide molecule to hybridize under said highly stringent wash conditions to said nucleic acid sequence when present in said sample; and
- (d) detecting any hybridized oligonucleotide molecules, wherein detection of said hybridized oligonucleotide molecules indicates the presence of said *E. coli* in said sample.

Claim 108. (Previously presented) The method as claimed in Claim 107, wherein step (b) involves providing one pair of oligonucleotide molecules, and wherein at least one oligonucleotide molecule of said pair hybridizes to one of said nucleic acid sequence.

Claim 109. (Previously presented) The method as claimed in Claim 108, wherein said pair of oligonucleotide molecules is a pair of polymerase chain reaction primers.

Claim 110. (Previously presented) The method as claimed in Claim 107, wherein said at least one oligonucleotide molecule is selected from the group consisting of positions 739-757 of SEQ ID NO:1, positions 925-942 of SEQ ID NO:1, positions 1165-1182 of SEQ ID NO:1, positions 8646-8663 of SEQ ID NO:1,

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positions 8906-8923 of SEQ ID NO:1, positions 9150-9167 of SEQ ID NO:1, positions 9976-9996 of SEQ ID NO:1, positions 10113-10130 of SEQ ID NO:1, positions 11821-11844 of SEQ ID NO:1, positions 12042-10259 of SEQ ID NO:1, positions 12258-12275 of SEQ ID NO:1, positions 1941-1924 of SEQ ID NO:1, positions 1731-1714 of SEQ ID NO:1, positions 1347-1330 of SEQ ID NO:1, positions 9908-9891 of SEQ ID NO:1, positions 9468-9451 of SEQ ID NO:1, positions 9754-9737 of SEQ ID NO:1, positions 10827-10807 of SEQ ID NO:1, positions 10484-10467 of SEQ ID NO:1, positions 12945-12924 of SEQ ID NO:1, positions 12447-12430 of SEQ ID NO:1 and positions 12698-12681 of SEQ ID NO:1.

Claim 111. (Previously presented) A method of testing a sample for the presence of *E. coli* encoding bacterial polysaccharide O-antigen serotype 0157, the method comprising the steps of:

- (a) providing a sample to be tested;
- (b) providing at least one oligonucleotide molecule which is about 17 to 28 nucleotides in length and hybridizes using highly stringent wash conditions, to a nucleic acid sequence selected from the group consisting of:

wbdN (nucleotide position 79 to 861 of SEQ ID NO:2);

wbdO (nucleotide positions 2011 to 2757 of SEQ ID NO:2);

wbdP (nucleotide positions 5365 to 6471 of SEQ ID NO:2);

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wbdR (nucleotide positions 13156 to 13821 of SEQ ID NO:2);

wzx (nucleotide positions 2744 to 3109 of SEQ ID NO:2); and

wzy (nucleotide positions 858 to 2042 of SEQ ID NO:2),

or to at least one nucleic acid sequence complementary to the group consisting of:

wbdN (nucleotide position 79 to 861 of SEQ ID NO:2);

wbdO (nucleotide positions 2011 to 2757 of SEQ ID NO:2);

wbdP (nucleotide positions 5365 to 6471 of SEQ ID NO:2);

wbdR (nucleotide positions 13156 to 13821 of SEQ ID NO:2);

wzx (nucleotide positions 2744 to 3109 of SEQ ID NO:2); and

wzy (nucleotide positions 858 to 2042 of SEQ ID NO:2),

- (c) contacting said sample with said at least one oligonucleotide molecule to permit said oligonucleotide molecule to hybridize under said highly stringent wash conditions to said nucleic acid sequence when present in said sample; and
- (d) detecting any hybridized oligonucleotide molecules, wherein detection of said hybridized oligonucleotide

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molecules indicates the presence of said *E. coli* in said sample.

Claim 112. (Previously presented) The method as claimed in Claim 111, wherein step (b) involves providing one pair of oligonucleotide molecules, and wherein at least one oligonucleotide molecule of said pair hybridizes to one of said nucleic acid sequence.

Claim 113. (Previously presented) The method as claimed in Claim 112, wherein said pair of oligonucleotide molecules is a pair of polymerase chain reaction primers.

Claim 114. (Previously presented) The method as claimed in Claim 111, wherein said at least one oligonucleotide molecule is selected from the group consisting of positions 79-96 of SEQ ID NO:2, positions 184-201 of SEQ ID NO:2, positions 310-327 of SEQ ID NO:2, positions 858-875 of SEQ ID NO:2, positions 1053-1070 of SEQ ID NO:2, positions 1278-1295 of SEQ ID NO:2, positions 2011-2028 of SEQ ID NO:2, positions 2110-2127 of SEQ ID NO:2, positions 2305-2322 of SEQ ID NO:2, positions 2744-2761 of SEQ ID NO:2, positions 2942-2959 of SEQ ID NO:2, positions 5440-5457 of SEQ ID NO:2, positions 5707-5724 of SEQ ID NO:2, positions 13261-13278 of SEQ ID NO:2, positions 13384-13401 of SEQ ID NO:2, positions 861-844 of SEQ ID NO:2, positions 531-514 of SEQ ID NO:2, positions 768-751 of SEQ ID NO:2, positions 2042-2025 of SEQ ID NO:2, positions 1619-1602 of SEQ ID NO:2, positions 1913-1896 of SEQ ID NO:2, positions 2757-2740 of SEQ ID NO:2, positions 2493-2476 of SEQ ID NO:2, positions 2682-2665 of SEQ ID NO:2, positions 6471-6454 of SEQ ID NO:2, positions 5973-5956 of SEQ

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ID NO:2, positions 6231-6214 of SEQ ID NO:2, positions 13629-13612 of SEQ ID NO:2 and positions 13731-13714 of SEQ ID NO:2.

Claim 115. (Previously presented) A method of testing a sample for the presence of *S. enterica* encoding bacterial polysaccharide O-antigen serotype C2, the method comprising the steps of:

- (a) providing a sample to be tested;
- (b) providing at least one oligonucleotide molecule which is about 17 to 28 nucleotides in length, and hybridizes using highly stringent wash conditions, to a nucleic acid sequence selected from the group consisting of:

wbaR (nucleotide positions at 2352 to 3314 of SEQ ID NO:3);

wbaL (nucleotide positions 3361 to 3875 of SEQ ID NO:3);

wbaQ (nucleotide positions 3977 to 5020 of SEQ ID NO:3);

wbaW (nucleotide positions 6313 to 7323 of SEQ ID NO:3);

wbaZ (nucleotide positions 7310 to 8467 of SEQ ID NO:3);

wzx (nucleotide positions 1019 to 2359 of SEQ ID NO:3); and

wzy (nucleotide positions 5114 to 6313 of SEQ ID NO:3),

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or to at least one nucleic acid sequence complementary to the group consisting of:

wbaR (nucleotide positions at 2352 to 3314 of SEQ ID NO:3);

wbaL (nucleotide positions 3361 to 3875 of SEQ ID NO:3);

wbaQ (nucleotide positions 3977 to 5020 of SEQ ID NO:3);

wbaW (nucleotide positions 6313 to 7323 of SEQ ID NO:3);

wbaZ (nucleotide positions 7310 to 8467 of SEQ ID NO:3);

wzx (nucleotide positions 1019 to 2359 of SEQ ID NO:3); and

wzy (nucleotide positions 5114 to 6313 of SEQ ID NO:3),

- (c) contacting said sample with said at least one oligonucleotide molecule to permit said oligonucleotide molecule to hybridize under said highly stringent wash conditions to said nucleic acid sequence when present in said sample; and
- (d) detecting any hybridized oligonucleotide molecules, wherein detection of said hybridized oligonucleotide molecules indicates the presence of said *S. enteria* in said sample.

Claim 116. (Previously presented) The method as claimed in Claim 115, wherein step (b) involves providing one pair of oligonucleotide molecules, and wherein at least one

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oligonucleotide molecule of the pair hybridizes to one of said nucleic acid sequence.

Claim 117. (Previously presented) The method as claimed in Claim 116, wherein said pair of oligonucleotide molecules is a pair of polymerase chain reaction primers.

Claim 118. (Previously presented) The method as claimed in Claim 115, wherein said at least one oligonucleotide molecule is selected from the group consisting of positions 1019-1036 of SEQ ID NO:3, positions 1708-1725 of SEQ ID NO:3, positions 1938-1955 of SEQ ID NO:3, positions 2352-2369 of SEQ ID NO:3, positions 2601-2618 of SEQ ID NO:3, positions 2910-2927 of SEQ ID NO:3, positions 3361-3378 of SEQ ID NO:3, positions 3578-3595 of SEQ ID NO:3, positions 3977-3994 of SEQ ID NO:3, positions 4167-4184 of SEQ ID NO:3, positions 4603-4620 of SEQ ID NO:3, positions 5114-5131 of SEQ ID NO:3, positions 5664-5681 of SEQ ID NO:3, positions 5907-5924 of SEQ ID NO:3, positions 6313-6330 of SEQ ID NO:3, positions 6697-6714 of SEQ ID NO:3, positions 6905-6922 of SEQ ID NO:3, positions 7310-7327 of SEQ ID NO:3, positions 7530-7547 of SEQ ID NO:3, positions 8007-8024 of SEQ ID NO:3, positions 1414-1397 of SEQ ID NO:3, positions 2170-2153 of SEQ ID NO:3, positions 2356-2339 of SEQ ID NO:3, positions 2759-2742 of SEQ ID NO:3, positions 3047-3030 of SEQ ID NO:3, positions 3311-3294 of SEQ ID NO:3, positions 3759-3742 of SEQ ID NO:3, positions 4378-4361 of SEQ ID NO:3, positions 4774-4757 of SEQ ID NO:3, positions 5017-5000 of SEQ ID NO:3, positions 5515-5498 of SEQ ID NO:3, positions 6112-6095 of SEQ ID NO:3, positions 6310-6293 of SEQ ID NO:3, positions 6805-6788 of SEQ ID NO:3, positions 7068-7051

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of SEQ ID NO:3, positions 7320-7303 of SEQ ID NO:3, positions 7775-7758 of SEQ ID NO:3, positions 7907-7890 of SEQ ID NO:3 and positions 8464-8447 of SEQ ID NO:3.

Claim 119. (Previously presented) A method of testing a sample for the presence of *S. enterica* encoding bacterial polysaccharide O-antigen serotype B, the method comprising the steps:

- (a) providing a sample to be tested;
- (b) providing at least one oligonucleotide molecule which is about 17 to 28 nucleotides in length and hybridizes using highly stringent wash conditions to a nucleic acid sequence selected from the group consisting of:

wzx (nucleotide positions 12762 to 14054 of
SEQ ID NO: 4); and
wbaV (nucleotide positions 14059 to 15060 of
SEQ ID NO: 4),

or to at least one nucleic acid sequence complementary to the group consisting of:

wzx (nucleotide positions 12762 to 14054 of
SEQ ID NO: 4); and
wbaV (nucleotide positions 14059 to 15060 of
SEQ ID NO: 4),

- (c) contacting said sample with said at least one oligonucleotide molecule to permit said oligonucleotide molecule to hybridize under said highly stringent wash conditions to said nucleic acid sequence when present in said genomic DNA; and

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- (d) detecting any hybridized oligonucleotide molecules, wherein detection of said hybridized oligonucleotide molecules indicates the presence of said *S. enteria* in said samples.

Claim 120. (Previously presented) The method as claimed in Claim 119, wherein step (b) involves providing one pair of oligonucleotide molecules, and wherein at least one oligonucleotide molecule of said pair hybridizes to one of said nucleic acid sequence.

Claim 121. (Previously presented) The method as claimed in Claim 120, wherein said pair of oligonucleotide molecules is a pair of polymerase chain reaction primers.

Claim 122. (Previously presented) The method as claimed in Claim 119, wherein said at least one oligonucleotide molecule is selected from the group consisting of positions 12762-12779 of SEQ ID NO:4, positions 12993-13010 of SEQ ID NO:4, positions 13635-13652 of SEQ ID NO:4, positions 14059-14076 of SEQ ID NO:4, positions 14688-14705 of SEQ ID NO:4, positions 13150-13133 of SEQ ID 140:4, positions 13417-13400 of SEQ ID NO:4, positions 14051-14034 of SEQ ID NO:4, positions 14421-14404 of SEQ ID NO:4, and positions 15057-15040 of SEQ ID NO:4.

Claim 123. (Previously presented) The method as claimed in any one of Claims 107, 111, 115 or 119, wherein the method further comprises providing at least one further oligonucleotide molecule, said further oligonucleotide molecule hybridizes using highly stringent wash conditions to a sugar-pathway gene specific to the bacterial strain to be detected, wherein said

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sugar-pathway gene is selected from the group consisting of *rmlB*, *rmlD*, *rmlA*, *rmlC*, *gtf*, *manC*, *manB*, *ddhD*, *ddhA*, *ddhB*, *ddhC* and *abe*, and contacting said further oligonucleotide molecule with said sample to permit said further oligonucleotide molecule to hybridize under said highly stringent wash conditions to said sugar-pathway gene, and detecting any specifically hybridized oligonucleotide molecules.

Claim 124. (Previously presented) The method according to any one of Claims 107, 111, 115 or 119, wherein the hybridized oligonucleotide molecules are detected by Southern blot analysis.

Claim 125. (Previously presented) The method as claimed in any one of Claims 109, 113, 117 or 121, wherein the method is performed using a polymerase chain reaction.

Claim 126. (Previously presented) The method as claimed in any one of Claims 107, 111, 115 or 119, wherein said sample is a food derived sample.

Claim 127. (Previously presented) The method as claimed in any one of Claims 107, 111, 115 or 119, wherein said sample is a faecal derived sample.

Claim 128. (Previously presented) The method as claimed in any one of Claims 107, 111, 115 or 119, wherein said sample is derived from a patient.